

SEQUENCE LISTING

<110> NG, Mary Mah Lee
CHU, Justin Jang Hann

<120> Molecules, Compositions, Methods and Kits For Applications
Associated With Flaviviruses

<130> 59419-010100

<140> to be assigned
<141> 2004-01-22

<150> US 60/442,157
<151> 2003-01-22

<160> 19

<170> PatentIn version 3.2

<210> 1
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<212> PRT
<213> Vero cells

<220>

<221> misc_feature
<222> (10)..(10)
<223> Xaa can be any naturally occurring amino acid

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Asp Thr Pro Lys Leu Glu Ile Ala Gly Xaa Phe Lys Asp Leu
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<210> 2
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Met Lys Thr Cys
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<210> 5

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Asp Pro Asn Val
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Arg Phe Asp Ser
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<211> 5

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Gly Arg Gly Asp Ser
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<210> 8

<211> 3147

<212> DNA

<213> Homo Sapiens

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<221> CDS

<222> (1)...(3144)

<223> Sequence coding for integrin alpha V subunit

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ccg ctt ctt ctc tcg gga ctc ctg cta cct ctg tgc cgc gcc ttc aac 96
 Pro Leu Leu Leu Ser Gly Leu Leu Leu Pro Leu Cys Arg Ala Phe Asn
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cta gac gtg gac agt cct gcc gag tac tct ggc ccc gag gga agt tac 144
 Leu Asp Val Asp Ser Pro Ala Glu Tyr Ser Gly Pro Glu Gly Ser Tyr
 35 40 45

ttc ggc ttc gcc gtg gat ttc ttc gtg ccc agc gcg tct tcc cgg atg 192
 Phe Gly Phe Ala Val Asp Phe Val Pro Ser Ala Ser Ser Arg Met
 50 55 60

ttt ctt ctc gtg gga gct ccc aaa gca aac acc acc cag cct ggg att 240
 Phe Leu Leu Val Gly Ala Pro Lys Ala Asn Thr Thr Gln Pro Gly Ile
 65 70 75 80

gtg gaa gga ggg cag gtc ctc aaa tgt gac tgg tct tct acc cgc cgg 288
 Val Glu Gly Gly Gln Val Leu Lys Cys Asp Trp Ser Ser Thr Arg Arg
 85 90 95

tgc cag cca att gaa ttt gat gca aca ggc aat aga gat tat gcc aag 336
 Cys Gln Pro Ile Glu Phe Asp Ala Thr Gly Asn Arg Asp Tyr Ala Lys
 100 105 110

gat gat cca ttg gaa ttt aag tcc cat cag tgg ttt gga gca tct gtg 384
 Asp Asp Pro Leu Glu Phe Lys Ser His Gln Trp Phe Gly Ala Ser Val
 115 120 125

agg tcg aaa cag gat aaa att ttg gcc tgt gcc cca ttg tac cat tgg 432
 Arg Ser Lys Gln Asp Lys Ile Leu Ala Cys Ala Pro Leu Tyr His Trp
 130 135 140

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 Arg Thr Glu Met Lys Gln Glu Arg Glu Pro Val Gly Thr Cys Phe Leu

145	150	155	160	
caa gat gga aca aag act gtt gag tat gct cca tgt aga tca caa gat Gln Asp Gly Thr Lys Thr Val Glu Tyr Ala Pro Cys Arg Ser Gln Asp				528
165	170	175		
att gat gct gat gga cag gga ttt tgt caa gga gga ttc agc att gat Ile Asp Ala Asp Gly Gln Gly Phe Cys Gln Gly Phe Ser Ile Asp				576
180	185	190		
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195	200	205		
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210	215	220		
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225	230	235	240	
cgg act gca caa gct att ttt gat gac agc tat ttg ggt tat tct gtg Arg Thr Ala Gln Ala Ile Phe Asp Asp Ser Tyr Leu Gly Tyr Ser Val				768
245	250	255		
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260	265	270		
gtt cca aga gca gca agg act ttg gga atg gtt tat att tat gat ggg Val Pro Arg Ala Ala Arg Thr Leu Gly Met Val Tyr Ile Tyr Asp Gly				864
275	280	285		
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290	295	300		
tat ttc gga ttt tct gta gct gcc act gac att aat gga gat gat tat Tyr Phe Gly Phe Ser Val Ala Ala Thr Asp Ile Asn Gly Asp Asp Tyr				960
305	310	315	320	
gca gat gtg ttt att gga gca cct ctc ttc atg gat cgt ggc tct gat Ala Asp Val Phe Ile Gly Ala Pro Leu Phe Met Asp Arg Gly Ser Asp				1008
325	330	335		
ggc aaa ctc caa gag gtg ggg cag gtc tca gtg tct cta cag aga gct Gly Lys Leu Gln Glu Val Gly Gln Val Ser Val Ser Leu Gln Arg Ala				1056
340	345	350		
tca gga gac ttc cag acg aca aag ctg aat gga ttt gag gtc ttt gca Ser Gly Asp Phe Gln Thr Thr Lys Leu Asn Gly Phe Glu Val Phe Ala				1104
355	360	365		
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370	375	380		

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gga att gtt tat atc ttc aat gga aga tca aca ggc ttg aac gca gtc Gly Ile Val Tyr Ile Phe Asn Gly Arg Ser Thr Gly Leu Asn Ala Val 405 410 415	1248
cca tct caa atc ctt gaa ggg cag tgg gct gct cga agc atg cca cca Pro Ser Gln Ile Leu Glu Gly Gln Trp Ala Ala Arg Ser Met Pro Pro 420 425 430	1296
agc ttt ggc tat tca atg aaa gga gcc aca gat ata gac aaa aat gga Ser Phe Gly Tyr Ser Met Lys Gly Ala Thr Asp Ile Asp Lys Asn Gly 435 440 445	1344
tat cca gac tta att gta gga gct ttt ggt gta gat cga gct atc tta Tyr Pro Asp Leu Ile Val Gly Ala Phe Gly Val Asp Arg Ala Ile Leu 450 455 460	1392
tac agg gcc aga cca gtt atc act gta aat gct ggt ctt gaa gtg tac Tyr Arg Ala Arg Pro Val Ile Thr Val Asn Ala Gly Leu Glu Val Tyr 465 470 475 480	1440
cct agc att tta aat caa gac aat aaa acc tgc tca ctg cct gga aca Pro Ser Ile Leu Asn Gln Asp Asn Lys Thr Cys Ser Leu Pro Gly Thr 485 490 495	1488
gct ctc aaa gtt tcc tgt ttt aat gtt agg ttc tgc tta aag gca gat Ala Leu Lys Val Ser Cys Phe Asn Val Arg Phe Cys Leu Lys Ala Asp 500 505 510	1536
ggc aaa gga gta ctt ccc agg aaa ctt aat ttc cag gtg gaa ctt ctt Gly Lys Gly Val Leu Pro Arg Lys Leu Asn Phe Gln Val Glu Leu Leu 515 520 525	1584
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gga ctg atg cag tgt gag gaa ttg ata gcg tat ctg cgg gat gaa tct Gly Leu Met Gln Cys Glu Leu Ile Ala Tyr Leu Arg Asp Glu Ser 565 570 575	1728
gaa ttt aga gac aaa ctc act cca att act att ttt atg gaa tat cgg Glu Phe Arg Asp Lys Leu Thr Pro Ile Thr Ile Phe Met Glu Tyr Arg 580 585 590	1776
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ttg att gtt aag gct cag aat caa gga gaa ggt gcc tac gaa gct gag Leu Ile Val Lys Ala Gln Asn Gln Gly Glu Gly Ala Tyr Glu Ala Glu 660 665 670	2016
ctc atc gtt tcc att cca ctg cag gct gat ttc atc ggg gtt gtc cga Leu Ile Val Ser Ile Pro Leu Gln Ala Asp Phe Ile Gly Val Val Arg 675 680 685	2064
aac aat gaa gcc tta gca aga ctt tcc tgt gca ttt aag aca gaa aac Asn Asn Glu Ala Leu Ala Arg Leu Ser Cys Ala Phe Lys Thr Glu Asn 690 695 700	2112
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Tyr Asn Asn Asn Thr Leu Leu Tyr Ile Leu His Tyr Asp Ile Asp Gly			
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cca atg aac tgc act tca gat atg gag atc aac cct ttg aga att aag			2592
Pro Met Asn Cys Thr Ser Asp Met Glu Ile Asn Pro Leu Arg Ile Lys			
850	855	860	
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Ile Ser Ser Leu Gln Thr Thr Glu Lys Asn Asp Thr Val Ala Gly Gln			
865	870	875	880
ggt gag cgg gac cat ctc atc act aag cgg gat ctt gcc ctc agt gaa			2688
Gly Glu Arg Asp His Leu Ile Thr Lys Arg Asp Leu Ala Leu Ser Glu			
885	890	895	
gga gat att cac act ttg ggt tgg gga gtt gct cag tgc ttg aag att			2736
Gly Asp Ile His Thr Leu Gly Cys Gly Val Ala Gln Cys Leu Lys Ile			
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gtc tgc caa gtt ggg aga tta gac aga gga aag agt gca atc ttg tac			2784
Val Cys Gln Val Gly Arg Leu Asp Arg Gly Lys Ser Ala Ile Leu Tyr			
915	920	925	
gta aag tca tta ctg tgg act gag act ttt atg aat aaa gaa aat cag			2832
Val Lys Ser Leu Leu Trp Thr Glu Thr Phe Met Asn Lys Glu Asn Gln			
930	935	940	
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Asn His Ser Tyr Ser Leu Lys Ser Ser Ala Ser Phe Asn Val Ile Glu			
945	950	955	960
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Phe Pro Tyr Lys Asn Leu Pro Ile Glu Asp Ile Thr Asn Ser Thr Leu			
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Val Thr Thr Asn Val Thr Trp Gly Ile Gln Pro Ala Pro Met Pro Val			
980	985	990	
cct gtg tgg gtg atc att tta gca gtt cta gca gga ttg ttg cta ctg			3024
Pro Val Trp Val Ile Ile Leu Ala Val Leu Ala Gly Leu Leu Leu			
995	1000	1005	
gct gtt ttg gta ttt gta atg tac agg atg ggc ttt ttt aaa cgg			3069
Ala Val Leu Val Phe Val Met Tyr Arg Met Gly Phe Phe Lys Arg			
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gtc cgg cca cct caa gaa gaa caa gaa agg gag cag ctt caa cct			3114
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<211> 1048

<212> PRT

<213> Homo Sapiens

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Leu Asp Val Asp Ser Pro Ala Glu Tyr Ser Gly Pro Glu Gly Ser Tyr
35 40 45

Phe Gly Phe Ala Val Asp Phe Phe Val Pro Ser Ala Ser Ser Arg Met
50 55 60

Phe Leu Leu Val Gly Ala Pro Lys Ala Asn Thr Thr Gln Pro Gly Ile
65 70 75 80

Val Glu Gly Gly Gln Val Leu Lys Cys Asp Trp Ser Ser Thr Arg Arg
85 90 95

Cys Gln Pro Ile Glu Phe Asp Ala Thr Gly Asn Arg Asp Tyr Ala Lys
100 105 110

Asp Asp Pro Leu Glu Phe Lys Ser His Gln Trp Phe Gly Ala Ser Val
115 120 125

Arg Ser Lys Gln Asp Lys Ile Leu Ala Cys Ala Pro Leu Tyr His Trp
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180 185 190

Phe Thr Lys Ala Asp Arg Val Leu Leu Gly Gly Pro Gly Ser Phe Tyr
195 200 205

Trp Gln Gly Gln Leu Ile Ser Asp Gln Val Ala Glu Ile Val Ser Lys
210 215 220

Tyr Asp Pro Asn Val Tyr Ser Ile Lys Tyr Asn Asn Gln Leu Ala Thr
225 230 235 240

Arg Thr Ala Gln Ala Ile Phe Asp Asp Ser Tyr Leu Gly Tyr Ser Val
245 250 255

Ala Val Gly Asp Phe Asn Gly Asp Gly Ile Asp Asp Phe Val Ser Gly
260 265 270

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275 280 285

Lys Asn Met Ser Ser Leu Tyr Asn Phe Thr Gly Glu Gln Met Ala Ala
290 295 300

Tyr Phe Gly Phe Ser Val Ala Ala Thr Asp Ile Asn Gly Asp Asp Tyr
305 310 315 320

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325 330 335

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340 345 350

Ser Gly Asp Phe Gln Thr Thr Lys Leu Asn Gly Phe Glu Val Phe Ala
355 360 365

Arg Phe Gly Ser Ala Ile Ala Pro Leu Gly Asp Leu Asp Gln Asp Gly
370 375 380

Phe Asn Asp Ile Ala Ile Ala Ala Pro Tyr Gly Gly Glu Asp Lys Lys
385 390 395 400

Gly Ile Val Tyr Ile Phe Asn Gly Arg Ser Thr Gly Leu Asn Ala Val
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420 425 430

Ser Phe Gly Tyr Ser Met Lys Gly Ala Thr Asp Ile Asp Lys Asn Gly
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Tyr Pro Asp Leu Ile Val Gly Ala Phe Gly Val Asp Arg Ala Ile Leu
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Tyr Arg Ala Arg Pro Val Ile Thr Val Asn Ala Gly Leu Glu Val Tyr
465 470 475 480

Pro Ser Ile Leu Asn Gln Asp Asn Lys Thr Cys Ser Leu Pro Gly Thr
485 490 495

Ala Leu Lys Val Ser Cys Phe Asn Val Arg Phe Cys Leu Lys Ala Asp
500 505 510

Gly Lys Gly Val Leu Pro Arg Lys Leu Asn Phe Gln Val Glu Leu Leu
515 520 525

Leu Asp Lys Leu Lys Gln Lys Gly Ala Ile Arg Arg Ala Leu Phe Leu
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Tyr Ser Arg Ser Pro Ser His Ser Lys Asn Met Thr Ile Ser Arg Gly
545 550 555 560

Gly Leu Met Gln Cys Glu Glu Leu Ile Ala Tyr Leu Arg Asp Glu Ser
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Glu Phe Arg Asp Lys Leu Thr Pro Ile Thr Ile Phe Met Glu Tyr Arg
580 585 590

Leu Asp Tyr Arg Thr Ala Ala Asp Thr Thr Gly Leu Gln Pro Ile Leu
595 600 605

Asn Gln Phe Thr Pro Ala Asn Ile Ser Arg Gln Ala His Ile Leu Leu
610 615 620

Asp Cys Gly Glu Asp Asn Val Cys Lys Pro Lys Leu Glu Val Ser Val
625 630 635 640

Asp Ser Asp Gln Lys Lys Ile Tyr Ile Gly Asp Asp Asn Pro Leu Thr
645 650 655

Leu Ile Val Lys Ala Gln Asn Gln Gly Glu Gly Ala Tyr Glu Ala Glu

660

665

670

Leu Ile Val Ser Ile Pro Leu Gln Ala Asp Phe Ile Gly Val Val Arg
675 680 685

Asn Asn Glu Ala Leu Ala Arg Leu Ser Cys Ala Phe Lys Thr Glu Asn
690 695 700

Gln Thr Arg Gln Val Val Cys Asp Leu Gly Asn Pro Met Lys Ala Gly
705 710 715 720

Thr Gln Leu Leu Ala Gly Leu Arg Phe Ser Val His Gln Gln Ser Glu
725 730 735

Met Asp Thr Ser Val Lys Phe Asp Leu Gln Ile Gln Ser Ser Asn Leu
740 745 750

Phe Asp Lys Val Ser Pro Val Val Ser His Lys Val Asp Leu Ala Val
755 760 765

Leu Ala Ala Val Glu Ile Arg Gly Val Ser Ser Pro Asp His Ile Phe
770 775 780

Leu Pro Ile Pro Asn Trp Glu His Lys Glu Asn Pro Glu Thr Glu Glu
785 790 795 800

Asp Val Gly Pro Val Val Gln His Ile Tyr Glu Leu Arg Asn Asn Gly
805 810 815

Pro Ser Ser Phe Ser Lys Ala Met Leu His Leu Gln Trp Pro Tyr Lys
820 825 830

Tyr Asn Asn Asn Thr Leu Leu Tyr Ile Leu His Tyr Asp Ile Asp Gly
835 840 845

Pro Met Asn Cys Thr Ser Asp Met Glu Ile Asn Pro Leu Arg Ile Lys
850 855 860

Ile Ser Ser Leu Gln Thr Thr Glu Lys Asn Asp Thr Val Ala Gly Gln
865 870 875 880

Gly Glu Arg Asp His Leu Ile Thr Lys Arg Asp Leu Ala Leu Ser Glu
885 890 895

Gly Asp Ile His Thr Leu Gly Cys Gly Val Ala Gln Cys Leu Lys Ile
900 905 910

Val Cys Gln Val Gly Arg Leu Asp Arg Gly Lys Ser Ala Ile Leu Tyr
915 920 925

Val Lys Ser Leu Leu Trp Thr Glu Thr Phe Met Asn Lys Glu Asn Gln
930 935 940

Asn His Ser Tyr Ser Leu Lys Ser Ser Ala Ser Phe Asn Val Ile Glu
945 950 955 960

Phe Pro Tyr Lys Asn Leu Pro Ile Glu Asp Ile Thr Asn Ser Thr Leu
965 970 975

Val Thr Thr Asn Val Thr Trp Gly Ile Gln Pro Ala Pro Met Pro Val
980 985 990

Pro Val Trp Val Ile Ile Leu Ala Val Leu Ala Gly Leu Leu Leu
995 1000 1005

Ala Val Leu Val Phe Val Met Tyr Arg Met Gly Phe Phe Lys Arg
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Val Arg Pro Pro Gln Glu Glu Gln Glu Arg Glu Gln Leu Gln Pro
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His Glu Asn Gly Glu Gly Asn Ser Glu Thr
1040 1045

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<223> Sequence coding for integrin beta 3 subunit

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ggg acc aca gtt ggg gtt ctg tcc atg gat tcc agc aat gtc ctc cag Gly Thr Thr Val Gly Val Leu Ser Met Asp Ser Ser Asn Val Leu Gln 355 360 365	1104
ctc att gtt gat gct tat ggg aaa atc cgt tct aaa gta gag ctg gaa Leu Ile Val Asp Ala Tyr Gly Lys Ile Arg Ser Lys Val Glu Leu Glu 370 375 380	1152
gtg cgt gac ctc cct gaa gag ttg tct cta tcc ttc aat gcc acc tgc Val Arg Asp Leu Pro Glu Glu Leu Ser Leu Ser Phe Asn Ala Thr Cys 385 390 395 400	1200
ctc aac aat gag gtc atc cct ggc ctc aag tct tgt atg gga ctc aag Leu Asn Asn Glu Val Ile Pro Gly Leu Lys Ser Cys Met Gly Leu Lys 405 410 415	1248
att gga gac acg gtg agc ttc agc att gag gcc aag gtg cga ggc tgt Ile Gly Asp Thr Val Ser Phe Ser Ile Glu Ala Lys Val Arg Gly Cys 420 425 430	1296
ccc cag gag aag gag aag tcc ttt acc ata aag ccc gtg ggc ttc aag Pro Gln Glu Lys Glu Lys Ser Phe Thr Ile Lys Pro Val Gly Phe Lys 435 440 445	1344
gac agc ctg atc gtc cag gtc acc ttt gat tgt gac tgt gcc tgc cag Asp Ser Leu Ile Val Gln Val Thr Phe Asp Cys Asp Cys Ala Cys Gln 450 455 460	1392
gcc caa gct gaa cct aat agc cat cgc tgc aac aat ggc aat ggg acc	1440

Ala Gln Ala Glu Pro Asn Ser His Arg Cys Asn Asn Gly Asn Gly Thr			
465	470	475	480
ttt gag tgt ggg gta tgc cgt tgt ggg cct ggc tgg ctg gga tcc cag			1488
Phe Glu Cys Gly Val Cys Arg Cys Gly Pro Gly Trp Leu Gly Ser Gln			
485	490	495	
tgt gag tgc tca gag gag gac tat cgc cct tcc cag cag gac gaa tgc			1536
Cys Glu Cys Ser Glu Glu Asp Tyr Arg Pro Ser Gln Gln Asp Glu Cys			
500	505	510	
agc ccc cgg gag ggt cag ccc gtc tgc agc cag cgg ggc gag tgc ctc			1584
Ser Pro Arg Glu Gly Gln Pro Val Cys Ser Gln Arg Gly Glu Cys Leu			
515	520	525	
tgt ggt caa tgt gtc tgc cac agc agt gac ttt ggc aag atc acg ggc			1632
Cys Gly Gln Cys Val Cys His Ser Ser Asp Phe Gly Lys Ile Thr Gly			
530	535	540	
aag tac tgc gag tgt gac gac ttc tcc tgt gtc cgc tac aag ggg gag			1680
Lys Tyr Cys Glu Cys Asp Asp Phe Ser Cys Val Arg Tyr Lys Gly Glu			
545	550	555	560
atg tgc tca ggc cat ggc cag tgc agc tgt ggg gac tgc ctg tgt gac			1728
Met Cys Ser Gly His Gly Gln Cys Ser Cys Gly Asp Cys Leu Cys Asp			
565	570	575	
tcc gac tgg acc ggc tac tac tgc aac tgt acc acg cgt act gac acc			1776
Ser Asp Trp Thr Gly Tyr Tyr Cys Asn Cys Thr Thr Arg Thr Asp Thr			
580	585	590	
tgc atg tcc agc aat ggg ctg ctg tgc agc ggc cgc ggc aag tgt gaa			1824
Cys Met Ser Ser Asn Gly Leu Leu Cys Ser Gly Arg Gly Lys Cys Glu			
595	600	605	
tgt ggc agc tgt gtc tgt atc cag ccg ggc tcc tat ggg gac acc tgt			1872
Cys Gly Ser Cys Val Cys Ile Gln Pro Gly Ser Tyr Gly Asp Thr Cys			
610	615	620	
gag aag tgc ccc acc tgc cca gat gcc tgc acc ttt aag aaa gaa tgt			1920
Glu Lys Cys Pro Thr Cys Pro Asp Ala Cys Thr Phe Lys Lys Glu Cys			
625	630	635	640
gtg gag tgt aag aag ttt gac cgg gag ccc tac atg acc gaa aat acc			1968
Val Glu Cys Lys Phe Asp Arg Glu Pro Tyr Met Thr Glu Asn Thr			
645	650	655	
tgc aac cgt tac tgc cgt gac gag att gag tca gtg aaa gag ctt aag			2016
Cys Asn Arg Tyr Cys Arg Asp Glu Ile Glu Ser Val Lys Glu Leu Lys			
660	665	670	
gac act ggc aag gat gca gtg aat tgt acc tat aag aat gag gat gac			2064
Asp Thr Gly Lys Asp Ala Val Asn Cys Thr Tyr Lys Asn Glu Asp Asp			
675	680	685	
tgt gtc gtc aga ttc cag tac tat gaa gat tct agt gga aag tcc atc			2112
Cys Val Val Arg Phe Gln Tyr Tyr Glu Asp Ser Ser Gly Lys Ser Ile			

690	695	700	
ctg tat gtg gta gaa gag cca gag tgt ccc aag ggc cct gac atc ctg Leu Tyr Val Val Glu Glu Pro Glu Cys Pro Lys Gly Pro Asp Ile Leu 705 710 715 720			2160
gtg gtc ctg ctc tca gtg atg ggg gcc att ctg ctc att ggc ctt gcc Val Val Leu Leu Ser Val Met Gly Ala Ile Leu Leu Ile Gly Leu Ala 725 730 735			2208
gcc ctg ctc atc tgg aaa ctc ctc atc acc atc cac gac cga aaa gaa Ala Leu Leu Ile Trp Lys Leu Leu Ile Thr Ile His Asp Arg Lys Glu 740 745 750			2256
ttc gct aaa ttt gag gaa gaa cgc gcc aga gca aaa tgg gac aca gcc Phe Ala Lys Phe Glu Glu Arg Ala Arg Ala Lys Trp Asp Thr Ala 755 760 765			2304
aac aac cca ctg tat aaa gag gcc acg tct acc ttc acc aat atc acg Asn Asn Pro Leu Tyr Lys Glu Ala Thr Ser Thr Phe Thr Asn Ile Thr 770 775 780			2352
tac cgg ggc act taa Tyr Arg Gly Thr 785			2367
<p><210> 11 <211> 788 <212> PRT <213> Homo Sapiens</p> <p><400> 11</p>			
Met Arg Ala Arg Pro Arg Pro Arg Pro Leu Trp Ala Thr Val Leu Ala 1 5 10 15			
Leu Gly Ala Leu Ala Gly Val Gly Val Gly Gly Pro Asn Ile Cys Thr 20 25 30			
Thr Arg Gly Val Ser Ser Cys Gln Gln Cys Leu Ala Val Ser Pro Met 35 40 45			
Cys Ala Trp Cys Ser Asp Glu Ala Leu Pro Leu Gly Ser Pro Arg Cys 50 55 60			
Asp Leu Lys Glu Asn Leu Leu Lys Asp Asn Cys Ala Pro Glu Ser Ile 65 70 75 80			
Glu Phe Pro Val Ser Glu Ala Arg Val Leu Glu Asp Arg Pro Leu Ser 85 90 95			

Asp Lys Gly Ser Gly Asp Ser Ser Gln Val Thr Gln Val Ser Pro Gln
100 105 110

Arg Ile Ala Leu Arg Leu Arg Pro Asp Asp Ser Lys Asn Phe Ser Ile
115 120 125

Gln Val Arg Gln Val Glu Asp Tyr Pro Val Asp Ile Tyr Tyr Leu Met
130 135 140

Asp Leu Ser Tyr Ser Met Lys Asp Asp Leu Trp Ser Ile Gln Asn Leu
145 150 155 160

Gly Thr Lys Leu Ala Thr Gln Met Arg Lys Leu Thr Ser Asn Leu Arg
165 170 175

Ile Gly Phe Gly Ala Phe Val Asp Lys Pro Val Ser Pro Tyr Met Tyr
180 185 190

Ile Ser Pro Pro Glu Ala Leu Glu Asn Pro Cys Tyr Asp Met Lys Thr
195 200 205

Thr Cys Leu Pro Met Phe Gly Tyr Lys His Val Leu Thr Leu Thr Asp
210 215 220

Gln Val Thr Arg Phe Asn Glu Glu Val Lys Lys Gln Ser Val Ser Arg
225 230 235 240

Asn Arg Asp Ala Pro Glu Gly Gly Phe Asp Ala Ile Met Gln Ala Thr
245 250 255

Val Cys Asp Glu Lys Ile Gly Trp Arg Asn Asp Ala Ser His Leu Leu
260 265 270

Val Phe Thr Thr Asp Ala Lys Thr His Ile Ala Leu Asp Gly Arg Leu
275 280 285

Ala Gly Ile Val Gln Pro Asn Asp Gly Gln Cys His Val Gly Ser Asp
290 295 300

Asn His Tyr Ser Ala Ser Thr Thr Met Asp Tyr Pro Ser Leu Gly Leu
305 310 315 320

Met Thr Glu Lys Leu Ser Gln Lys Asn Ile Asn Leu Ile Phe Ala Val
325 330 335

Thr Glu Asn Val Val Asn Leu Tyr Gln Asn Tyr Ser Glu Leu Ile Pro
340 345 350

Gly Thr Thr Val Gly Val Leu Ser Met Asp Ser Ser Asn Val Leu Gln
355 360 365

Leu Ile Val Asp Ala Tyr Gly Lys Ile Arg Ser Lys Val Glu Leu Glu
370 375 380

Val Arg Asp Leu Pro Glu Glu Leu Ser Leu Ser Phe Asn Ala Thr Cys
385 390 395 400

Leu Asn Asn Glu Val Ile Pro Gly Leu Lys Ser Cys Met Gly Leu Lys
405 410 415

Ile Gly Asp Thr Val Ser Phe Ser Ile Glu Ala Lys Val Arg Gly Cys
420 425 430

Pro Gln Glu Lys Glu Lys Ser Phe Thr Ile Lys Pro Val Gly Phe Lys
435 440 445

Asp Ser Leu Ile Val Gln Val Thr Phe Asp Cys Asp Cys Ala Cys Gln
450 455 460

Ala Gln Ala Glu Pro Asn Ser His Arg Cys Asn Asn Gly Asn Gly Thr
465 470 475 480

Phe Glu Cys Gly Val Cys Arg Cys Gly Pro Gly Trp Leu Gly Ser Gln
485 490 495

Cys Glu Cys Ser Glu Glu Asp Tyr Arg Pro Ser Gln Gln Asp Glu Cys
500 505 510

Ser Pro Arg Glu Gly Gln Pro Val Cys Ser Gln Arg Gly Glu Cys Leu
515 520 525

Cys Gly Gln Cys Val Cys His Ser Ser Asp Phe Gly Lys Ile Thr Gly
530 535 540

Lys Tyr Cys Glu Cys Asp Asp Phe Ser Cys Val Arg Tyr Lys Gly Glu

545

550

555

560

Met Cys Ser Gly His Gly Gln Cys Ser Cys Gly Asp Cys Leu Cys Asp
565 570 575

Ser Asp Trp Thr Gly Tyr Tyr Cys Asn Cys Thr Thr Arg Thr Asp Thr
580 585 590

Cys Met Ser Ser Asn Gly Leu Leu Cys Ser Gly Arg Gly Lys Cys Glu
595 600 605

Cys Gly Ser Cys Val Cys Ile Gln Pro Gly Ser Tyr Gly Asp Thr Cys
610 615 620

Glu Lys Cys Pro Thr Cys Pro Asp Ala Cys Thr Phe Lys Lys Glu Cys
625 630 635 640

Val Glu Cys Lys Lys Phe Asp Arg Glu Pro Tyr Met Thr Glu Asn Thr
645 650 655

Cys Asn Arg Tyr Cys Arg Asp Glu Ile Glu Ser Val Lys Glu Leu Lys
660 665 670

Asp Thr Gly Lys Asp Ala Val Asn Cys Thr Tyr Lys Asn Glu Asp Asp
675 680 685

Cys Val Val Arg Phe Gln Tyr Tyr Glu Asp Ser Ser Gly Lys Ser Ile
690 695 700

Leu Tyr Val Val Glu Glu Pro Glu Cys Pro Lys Gly Pro Asp Ile Leu
705 710 715 720

Val Val Leu Leu Ser Val Met Gly Ala Ile Leu Leu Ile Gly Leu Ala
725 730 735

Ala Leu Leu Ile Trp Lys Leu Leu Ile Thr Ile His Asp Arg Lys Glu
740 745 750

Phe Ala Lys Phe Glu Glu Arg Ala Arg Ala Lys Trp Asp Thr Ala
755 760 765

Asn Asn Pro Leu Tyr Lys Glu Ala Thr Ser Thr Phe Thr Asn Ile Thr
770 775 780

Tyr Arg Gly Thr
785

<210> 12
<211> 64
<212> DNA
<213> Synthetic DNA

<220>
<221> misc_feature
<222> (1)..(64)
<223> Integrin sequence alpha V1

<400> 12
gatcccgaa ttgttatat cttcattcaa gagatgaaga tataaacaat tccttttg 60
gaaa 64

<210> 13
<211> 64
<212> DNA
<213> Synthetic DNA

<220>
<221> misc_feature
<222> (1)..(64)
<223> Integrin sequence alpha V2

<400> 13
gatcccgact ttcctgtgca tttattcaa gagattaaat gcacaggaaa gtcttttg 60
gaaa 64

<210> 14
<211> 63
<212> DNA
<213> Synthetic DNA

<220>
<221> misc_feature
<222> (1)..(63)
<223> Integrin sequence beta 31

<400> 14
gatcccacat caatttgcac tttgcttcaa gagagcaaag atcaaattga tgtttttg 60
aaa 63

<210> 15
 <211> 64
 <212> DNA
 <213> Synthetic DNA

<220>
 <221> misc_feature
 <222> (1)..(64)
 <223> Integrin sequence beta 32

<400> 15
 gatccgttgt acctataaga atgagttcaa gagactcatt cttataggta caatttttg 60
 gaaa 64

<210> 16
 <211> 1233
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)..(1233)
 <223> Sequence coding for neuropeptide Y receptor

<400> 16
 atg gaa acc agc agc ccg cgg ccc ccg cgg ccc agc tcc aac ccg ggg 48
 Met Glu Thr Ser Ser Pro Arg Pro Pro Arg Pro Ser Ser Asn Pro Gly
 1 5 10 15

ctg agc ctg gac gcc cgg ctg ggc gtg gac act cgc ctc tgg gcc aag 96
 Leu Ser Leu Asp Ala Arg Leu Gly Val Asp Thr Arg Leu Trp Ala Lys
 20 25 30

gtg ctg ttc acc gcg ctc tac gca ctc atc tgg gcg ctg ggc gcg gcg 144
 Val Leu Phe Thr Ala Leu Tyr Ala Leu Ile Trp Ala Leu Gly Ala Ala
 35 40 45

ggc aat gcg ctg tcc gtg cac gtg gtg ctg aag gcg cgg gcc ggg cgc 192
 Gly Asn Ala Leu Ser Val His Val Val Leu Lys Ala Arg Ala Gly Arg
 50 55 60

gcg ggg cgc ctg cgc cac cac gtg ctc agc ctg gcg ctc gcg ggc ctg 240
 Ala Gly Arg Leu Arg His His Val Leu Ser Leu Ala Leu Ala Gly Leu
 65 70 75 80

ctg ctg ctg gtc ggc gtg ccg gtg gag ctc tac agc ttc gtg tgg 288
 Leu Leu Leu Val Gly Val Pro Val Glu Leu Tyr Ser Phe Val Trp
 85 90 95

ttc cac tac ccc tgg gtc ttc ggc gac ctg ggc tgc cgc ggc tac tac 336
 Phe His Tyr Pro Trp Val Phe Gly Asp Leu Gly Cys Arg Gly Tyr Tyr
 100 105 110

ttc gtg cac gag ctg tgc gcc tac gcc acg gtg ctg agc gtg gca ggc Phe Val His Glu Leu Cys Ala Tyr Ala Thr Val Leu Ser Val Ala Gly 115 120 125	384
ctg agc gcc gag cgc tgc cta gcc gtg tgc cag ccc ctg cgt gcc cgc Leu Ser Ala Glu Arg Cys Leu Ala Val Cys Gln Pro Leu Arg Ala Arg 130 135 140	432
agc ctg ctg acg cca cgc cg acc cg tgg ctg gtg gcg ctc tcg tgg Ser Leu Leu Thr Pro Arg Arg Thr Arg Trp Leu Val Ala Leu Ser Trp 145 150 155 160	480
gcc gcc tcg ctc ggc ctc gcc ctg ccc atg gcc gtc atc atg ggg cag Ala Ala Ser Leu Gly Leu Ala Leu Pro Met Ala Val Ile Met Gly Gln 165 170 175	528
aag cac gaa ctc gag acg gcg gac ggg gag ccg gag ccc gcc tcg cga Lys His Glu Leu Glu Thr Ala Asp Gly Glu Pro Glu Pro Ala Ser Arg 180 185 190	576
gtg tgc acg gtg ctg gtg agc cgc acc gcg ctc caa gtc ttt atc cag Val Cys Thr Val Leu Val Ser Arg Thr Ala Leu Gln Val Phe Ile Gln 195 200 205	624
gtg aat gtg ctg gtg tcc ttc gtg ctc ccc ttg gca cta act gct ttc Val Asn Val Leu Val Ser Phe Val Leu Pro Leu Ala Leu Thr Ala Phe 210 215 220	672
ctg aat ggg gtc aca gtg agc cac ctg ctg gcc ctc tgc tcc caa gtg Leu Asn Gly Val Thr Val Ser His Leu Leu Ala Leu Cys Ser Gln Val 225 230 235 240	720
ccg tcc act tct acc ccg ggc agc tcc acc ccc agc cgc ctg gag ctg Pro Ser Thr Ser Pro Gly Ser Ser Thr Pro Ser Arg Leu Glu Leu 245 250 255	768
ctg agt gag gag ggt ctc ctc agc ttc atc gta tgg aag aag acc ttt Leu Ser Glu Glu Gly Leu Leu Ser Phe Ile Val Trp Lys Lys Thr Phe 260 265 270	816
atc cag gga ggc cag gtc agc ctg gtg aga cat aaa gac gtg cgc cgg Ile Gln Gly Gln Val Ser Leu Val Arg His Lys Asp Val Arg Arg 275 280 285	864
atc cgc agc ctc cag cgc agc gtc cag gtt ctc aga gcc atc gtg gtc Ile Arg Ser Leu Gln Arg Ser Val Gln Val Leu Arg Ala Ile Val Val 290 295 300	912
atg tat gtc atc tgc tgg ctg ccg tac cat gcc cgc agg ctc atg tac Met Tyr Val Ile Cys Trp Leu Pro Tyr His Ala Arg Arg Leu Met Tyr 305 310 315 320	960
tgc tac gta cct gat gac gcg tgg act gac cca ctg tac aat ttc tac Cys Tyr Val Pro Asp Asp Ala Trp Thr Asp Pro Leu Tyr Asn Phe Tyr 325 330 335	1008
cac tac ttc tac atg gtg acc aac aca ctt ttc tac gtc agc tca gct	1056

His Tyr Phe Tyr Met Val Thr Asn Thr Leu Phe Tyr Val Ser Ser Ala
 340 345 350

gtg act cct ctt ctc tac aac gcc gtg tcc tcc tcc aga aaa ctc 1104
 Val Thr Pro Leu Leu Tyr Asn Ala Val Ser Ser Phe Arg Lys Leu
 355 360 365

ttc ctg gaa gcc gtc agc tcc ctg tgt gga gag cac cac ccc atg aag 1152
 Phe Leu Glu Ala Val Ser Ser Leu Cys Gly Glu His His Pro Met Lys
 370 375 380

cgg tta ccc ccg aag ccc cag agt ccc acc cta atg gat aca gct tca 1200
 Arg Leu Pro Pro Lys Pro Gln Ser Pro Thr Leu Met Asp Thr Ala Ser
 385 390 395 400

ggc ttt ggg gat ccc cca gaa acc cgg acc tga 1233
 Gly Phe Gly Asp Pro Pro Glu Thr Arg Thr
 405 410

<210> 17
 <211> 410
 <212> PRT
 <213> Homo sapiens

<400> 17

Met Glu Thr Ser Ser Pro Arg Pro Pro Arg Pro Ser Ser Asn Pro Gly
 1 5 10 15

Leu Ser Leu Asp Ala Arg Leu Gly Val Asp Thr Arg Leu Trp Ala Lys
 20 25 30

Val Leu Phe Thr Ala Leu Tyr Ala Leu Ile Trp Ala Leu Gly Ala Ala
 35 40 45

Gly Asn Ala Leu Ser Val His Val Val Leu Lys Ala Arg Ala Gly Arg
 50 55 60

Ala Gly Arg Leu Arg His His Val Leu Ser Leu Ala Leu Ala Gly Leu
 65 70 75 80

Leu Leu Leu Val Gly Val Pro Val Glu Leu Tyr Ser Phe Val Trp
 85 90 95

Phe His Tyr Pro Trp Val Phe Gly Asp Leu Gly Cys Arg Gly Tyr Tyr
 100 105 110

Phe Val His Glu Leu Cys Ala Tyr Ala Thr Val Leu Ser Val Ala Gly
 115 120 125

Leu Ser Ala Glu Arg Cys Leu Ala Val Cys Gln Pro Leu Arg Ala Arg
130 135 140

Ser Leu Leu Thr Pro Arg Arg Thr Arg Trp Leu Val Ala Leu Ser Trp
145 150 155 160

Ala Ala Ser Leu Gly Leu Ala Leu Pro Met Ala Val Ile Met Gly Gln
165 170 175

Lys His Glu Leu Glu Thr Ala Asp Gly Glu Pro Glu Pro Ala Ser Arg
180 185 190

Val Cys Thr Val Leu Val Ser Arg Thr Ala Leu Gln Val Phe Ile Gln
195 200 205

Val Asn Val Leu Val Ser Phe Val Leu Pro Leu Ala Leu Thr Ala Phe
210 215 220

Leu Asn Gly Val Thr Val Ser His Leu Leu Ala Leu Cys Ser Gln Val
225 230 235 240

Pro Ser Thr Ser Thr Pro Gly Ser Ser Thr Pro Ser Arg Leu Glu Leu
245 250 255

Leu Ser Glu Glu Gly Leu Leu Ser Phe Ile Val Trp Lys Lys Thr Phe
260 265 270

Ile Gln Gly Gly Gln Val Ser Leu Val Arg His Lys Asp Val Arg Arg
275 280 285

Ile Arg Ser Leu Gln Arg Ser Val Gln Val Leu Arg Ala Ile Val Val
290 295 300

Met Tyr Val Ile Cys Trp Leu Pro Tyr His Ala Arg Arg Leu Met Tyr
305 310 315 320

Cys Tyr Val Pro Asp Asp Ala Trp Thr Asp Pro Leu Tyr Asn Phe Tyr
325 330 335

His Tyr Phe Tyr Met Val Thr Asn Thr Leu Phe Tyr Val Ser Ser Ala
340 345 350

Val Thr Pro Leu Leu Tyr Asn Ala Val Ser Ser Ser Phe Arg Lys Leu
355 360 365

Phe Leu Glu Ala Val Ser Ser Leu Cys Gly Glu His His Pro Met Lys
370 375 380

Arg Leu Pro Pro Lys Pro Gln Ser Pro Thr Leu Met Asp Thr Ala Ser
385 390 395 400

Gly Phe Gly Asp Pro Pro Glu Thr Arg Thr
405 410

<210> 18

<211> 65

<212> DNA

<213> Synthetic DNA

<220>

<221> misc_feature

<222> (1)..(65)

<223> Functional sequence of neuropeptide Y receptor used for siRNA

<400> 18

gatcccggtta tgactttgg acagtcttca agagagactg tccaaaagtc ataattttt 60

ggaaaa

65

<210> 19

<211> 14

<212> PRT

<213> West Nile Virus

<220>

<221> misc_feature

<222> (10)..(10)

<223> Xaa can be any naturally occurring amino acid

<400> 19

Ser Ile Pro Lys Leu Glu Ile Ala Gly Xaa Phe Lys Asp Leu
1 5 10